the splice donor sites [DS1 (SEQ ID NOs: 36 and 38) and DS2 (SEQ ID NO: 39)] and acceptor sites [AS1 (SEQ ID NOs: 37 and 40), AS2 (SEQ ID NO: 41) and AS3 (SEQ ID NO: 42)];

the sequences obtained from the clone RG083M05, in the lower-case boxes, and the sequences derived from experimental placental clones (mRNA), in the upper-case boxes;

C2 cont'd

the putative ORFs (ORF1, ORF2 and ORF3); and

an insert of 2 Kb present in DNA form but not detected in RNA form, represented in the form of vertical hatches.

Page 16, line 30 - Page 17, line 5, delete current paragraph and insert therefor:

- Figure 5 represents the alignment of the 5' and 3' flanking regions of the clone RG083M05 [SEQ ID NO: 43 (5-RG-28000-28872) and SEQ ID NO: 44 (3-RG-37500-38314)] with the terminal 5' and/or 3' regions of some placental clones [SEQ ID NO: 45 (3-PH74.2358-2782), SEQ ID NO: 46 (3-C4C5.710-1136), SEQ ID NO: 47 (5-6A2.1-600), SEQ ID NO: 48 (5-PH74.1-530) and SEQ ID NO: 49 (5-24.4.1-486)]; the CAAC tandem flanking the 3' and 5' LTRs is doubly underlined under the DNA sequences, the consensus LTR sequence of 783 bp (base pairs) (SEQ ID NO: 15) is indicated under the alignment; the PPT upstream of the 5' end of LTR and the PBS downstream of the 3' end of LTR are indicated; the U3R and U5 regions are indicated; the sites corresponding to the binding of the transcription factor are underlined and numbered from 1 to 6; the region -73 to 284 corresponds to the sequence evaluated in "CAT assay"; * corresponds to putative sites for "capping"; [polyA] indicates the polyadenylation signal.

C3

Page 17, lines 6-19, delete current paragraph and insert therefor:

C4

- Figure 6 represents a putative sequence of a HERV-W envelope polypeptide (ORF1) (SEQ ID NO: 33) obtained from 3 different placental cDNA clones; the leader

peptide (L), the surface protein (SU) and the transmembrane protein (TM) are indicated by arrows; the hydrophobic fusion peptide and the transmembrane carboxy region are underlined by a single line and a double line, respectively; the immunosuppression region is indicated in italics; the potential glycosylation sites are indicated by dots; the divergent amino acids are indicated on the bottom line; Figure 6 also presents the open reading frames corresponding to ORF2 (SEQ ID NO: 34) and ORF3 (SEQ ID NO: 35) as described in Figure 2, and more particularly the homologies of portions thereof (SEQ ID NOs: 50 and 51) with the retroviral regulatory genes (SEQ ID NOs: 52 and 53, respectively).

Page 21, line 35 - Page 22, line 20, delete current paragraph and insert therefor:

The reconstructed sequence (RNA) is integrally contained inside the genomic clone RG083M05 (9.6 Kb) and exhibits a 96% similarity with two discontinuous regions of this clone which also contains repeat regions at each end. The alignment of the experimental sequences corresponding to the 5' and 3' regions of the genomic RNA reconstructed with the DNA of the clone RG083M05 [5' (5-RG-28000-28872) (SEQ ID NO: 43) and 3' (3-RG-37500-38314) (SEQ ID NO: 44)] made it possible to deduce an LTR sequence and to identify elements characteristic of the retroviruses, in particular those involved in the reverse transcription, namely PBS downstream of the 5' LTR and the PPT upstream of the 3' LTR (cf Figure 5). It is observed that the U3 element is extremely short in comparison with that observed in the mammalian type C retroviruses, and is comparable in size to the U3 region generally described in the type D retroviruses and the avian retroviruses. The region corresponding to bases 2364 to 2720 of the clone cl.PH74 (SEQ ID NO: 7) was amplified by PCR and subcloned into the vector pCAT3 (Promega) in order to carry out the evaluation of the promoter activity. A significant activity was found in HeLa cells by the so-called "CAT assay" method showing the functionality of the promoter sequence of the LTR.